REMARKS/ARGUMENTS

The present amendment is submitted in accordance with the Revised Amendment Format as set forth in the Notice provided on the USPTO web site for the Office of Patent Legal Administration; Pre-OG Notices; signed 1/31/03.

1. Status of the claims

Claims 40, 67, 68 and 75 are amended and claim 65 is canceled. Claims 40 and 66-78 are currently pending with entry of the Amendment.

2. Support for the Amendments

Support for the amendments to the claims can be found throughout the specification, the drawings, and the claims as originally drafted. For example, support for the amendment to claim 40 and 75 can be found on, e.g., page 20, lines 17-34 (teaching the domains of AGL8), page 22, line 20 (teaching 75% identity) and page 50, line 26 (teaching fragments at least 50 base pairs for use in suppressing gene expression) of the specification. No new matter is added.

3. Interview

Applicants thank the Examiner for the helpful interview on July 11, 2003. Per the Examiner's request, Applicants have included a copy of the declaration regarding SaMADS filed in a different application.

4. Drawings

The Examiner objected to Figures 2, 5 and 8.

Specifically, the Examiner stated that the brief description indicated that Figure 2 was labeled "A-D," but the Figures did not contain the corresponding labels. To correct this issue, the description on page 8 is amended herein to omit reference to "A-D."

The Examiner also requested that Applicants insert labels "A" and "B" on Figure 5. Replacement drawings included herein contain the requested labels.

The Examiner also requested that Applicant add labels "a-f" to the figure. Applicants respectfully note that the figures already include those labels.

The Examiner also requested that Applicants clarify Figure 8. To expedite prosecution, Applicants have canceled Figure 8 and renumbered Figure 9 as Figure 8. Applicants note that the sequences provided in canceled Figure 8 are available in the sequence listing and the relationship of the depicted sequences is inherent.

5. Double patenting rejection

Claims 40 and 65-78 were provisionally rejected under the judicially-created doctrine of obviousness-type double patenting in view of Application No. 09/708,584, now U.S. Patent No. 6,541,683, issued April 1, 2003. Applicants will gladly provide a terminal disclaimer when the Examiner has indicated that the claims are otherwise allowable.

6. Rejections under 35 U.S.C. § 112, first paragraph: written description

Claims 40, 65 and 67-78 were rejected under 35 U.S.C. § 112, first paragraph as allegedly not fulfilling the written description requirement. In view of the interview, it is Applicants understanding that the amended claims overcome this rejection. Accordingly, Applicants respectfully request withdrawal of the rejection.

7. Rejections under 35 U.S.C. § 112, first paragraph: enablement

Claims 40, 65-74 were rejected under 35 U.S.C. § 112, first paragraph as allegedly not enabled. In view of the interview, it is Applicants understanding that the amended claims overcome this rejection. The amended claims involve introduction of an exogenous nucleic acid into a plant, thereby encompassing cosuppression and antisense methods. Accordingly, Applicants respectfully request withdrawal of the rejection.

8. Rejection under 35 U.S.C. § 102(b)

Claims 40, 65 and 66 were rejected as allegedly anticipated by, or obvious, in light of Mandel *et al.* (*Nature*) in view of Mandel *et al.* (*Plant Cell*). Specifically, the Examiner

argued that Mandel *et al.* (*Nature*) describes transformation of plants with AP1 and Mandel *et al.* (*Plant Cell*) state that AGL8 expression is inherently suppressed in AP1 transformants. Applicants respectfully traverse the rejection.

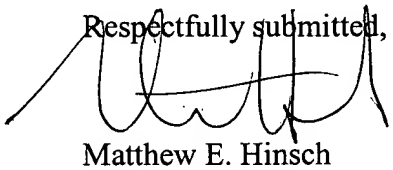
As amended, the claims are directed to plants transformed with a nucleic acid at least 50 base pairs long, wherein the nucleic acid encodes a polypeptide fragment at least 75% identical to the K, I or C domains of SEQ ID NO:1. Since AP1 is not greater than 75% identical to SEQ ID NO:2 in these domains, Mandel *et al.* (*Nature*) cannot anticipate the newly added claims. Accordingly, withdrawal of the rejection is requested.

CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



Matthew E. Hinsch
Reg. No. 47,651

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, 8th Floor
San Francisco, California 94111-3834
Tel: 415-576-0200
Fax: 415-576-0300
MEH:meh
SF 1476400 v1

PATENT
Our Docket: P-UD 3040

#13

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Yanofsky et al.	Group Art Unit: 1649
Serial No.: 09/105,652	Examiner: A. Mehta
Filed: June 26, 1998	
For: METHOD OF INCREASING FRUIT SIZE IN A PLANT	

Attention Box AF
Commissioner for Patents
Washington, D.C. 20231

DECLARATION UNDER 37 C.F.R. § 1.132

I, the undersigned, hereby declare as follows:

1. I am the Martin F. Yanofsky who is named as a co-inventor of the above-identified application with Robert Martienssen, Cristina Ferrandiz and Qing Gu.

2. I understand that the claims of the above-identified application stand rejected, in part, on the ground that *Sinapis alba* SaMADS B is not an ortholog of *Arabidopsis* AGL8. I understand that the claims of the above-identified application also stand rejected, in part, on the ground that the identification and use of AGL8 orthologs other than *Arabidopsis* AGL8 allegedly would have required an unreasonable amount of unpredictable experimentation.

3. Nucleic acid sequences encoding AGL8 orthologs were publicly available at the time of the invention. The nucleic acid sequence of the *Arabidopsis* AGL8 ortholog was publicly available at the time of the invention, as evidenced by my publication Mandel and Yanofsky, The Plant Cell, 7:1763-1771 (1995), attached hereto as Exhibit 1.

4. A nucleic acid molecule encoding the *Sinapis alba* ortholog of *Arabidopsis* AGL8, designated SaMADS B, also was publicly available at the time of the invention. The SaMADS B sequence was available in Menzel et al., Plant J. 9:399-408 (1996), attached as Exhibit 2. One skilled in the art would believe that SaMADS B was an ortholog of *Arabidopsis* AGL8 based, in part, on an alignment of the *Arabidopsis* AGL8 ("AGLP") and SaMADS B coding sequences showing that the two sequences are identical over the amino terminal 150 residues and differ by only eight amino acid substitutions (see Exhibit 3). Furthermore, BLAST analysis with the AGL8 coding sequence shows that the *Arabidopsis* AGL8 coding sequence is more similar to the *Sinapis alba* gene SaMADS B than to any other known sequence in GenBank (Exhibit 4). A phylogeny of the plant MADS box genes from Purugganan, J. Mol. Evol. 45:392-396 (1997), further demonstrates that SaMADS B is more closely related to *Arabidopsis* AGL8 than to any other known plant MADS box gene (Exhibit 5). Based on the high level of sequence conservation between these two genes and the fact that SaMADS B is more closely related to *Arabidopsis* AGL8 than to any other *Arabidopsis* gene, a plant molecular biologist would know that SaMADS B is the *Sinapis alba* ortholog of AGL8.

5. The consistent expression patterns of SaMADS B and AGL8 corroborate that these genes are orthologs. In particular, both genes are expressed in the shoot apex after photoinduction, as evidenced in the attached publications by Hempel et al. and Menzel et al., Exhibits 6 and 2, respectively (page 3849, column 2, and page 3950, Figure 5, of Hempel et al., Development 124:3845-3853 (1997); and Menzel et al., abstract; page 403, left column, first full paragraph). The photo-inducible expression in the shoot apex seen for both *AGL8* and *SaMADS B* corroborates the high degree of structural homology between these genes and confirms that SaMADS B is an ortholog of *Arabidopsis* AGL8.

6. Support for the routine identification and use of AGL8 orthologs other than *Arabidopsis* and *Sinapis alba* AGL8 is provided in paragraphs 7 to 10 and Exhibits 7 to 9 below. The results shown below corroborate that only routine techniques would have been required for a typical plant molecular biologist to clone a *Brassica* or non-*Brassica* ortholog of *Arabidopsis* AGL8. Specifically, the results shown below indicate that the AGL8 locus has been duplicated in maize, an occurrence which is common in this plant species. The results shown below further indicate that the two maize (*Zea mays*) orthologs of *Arabidopsis* AGL8 were cloned using routine molecular biology methods.

7. A phage cDNA library was prepared from maize ears using a cDNA synthesis and library construction kit from Stratagene. Two closely related cDNAs were isolated, Geo27 and Geo16. Based on the significant similarity between these two sequences, Geo27 and Geo16 appear to be gene products encoded by duplicated loci. Moreover, both Geo16 and Geo27 demonstrated about 50% identity at the amino acid level to *Arabidopsis* AGL8. Based on the high percentage homology and the fact that the Geo16 and Geo27 maize cDNAs were more similar to *Arabidopsis* AGL8 than to any other *Arabidopsis* gene, Geo16 and Geo27 are the maize orthologs of *Arabidopsis* AGL8. An alignment of the *Arabidopsis* AGL8 ("AGL8"); maize Geo16 and maize Geo27 amino acid sequences (ZAGL17) is shown in Exhibit 7. The nucleotide sequence of the maize AGL8 ortholog, Geo27, is shown in Exhibit 8.

8. Using routine cloning methods, the maize AGL8 cDNA, Geo27, was inserted into the BamHI site of vector pAHC17, a well known vector for directing constitutive high-level expression in maize under control of the maize ubiquitin promoter. The Geo27 vector was transformed into maize at the Iowa Plant Transformation facility using particle bombardment. About 78 first generation transformed lines were obtained that were positive for Geo27 by Southern analysis. By Northern analysis, approximately 18 of the transgenic lines were positive for Geo27 expression, with different lines expressing Geo27 at varying levels.

9. In these transformed lines, early results indicate that kernels of increased size are present in high-expressing maize AGL8 (Geo27) lines as compared to non-expressing lines. As evidence of the function of maize AGL8, Exhibit 9 shows increased kernel size in a transgenic ear expressing high levels of Geo27 as compared to a transgenic ear in which ectopic Geo27 expression was not evident.

10. In sum, these results confirm that additional AGL8 orthologs, including *Brassica* and non-Brassica orthologs, could be routinely isolated by a plant molecular biologist and that such orthologs retain the functional characteristics of *Arabidopsis* AGL8. Moreover, these results corroborate that the conserved function of AGL8 extends to monocot as well as dicot species.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that willful false statements may jeopardize the validity of the application or any patent issuing thereon.

May 9 2010
Date

Martin Yanofsky
Martin F. Yanofsky